

Appl. No. : 10/009,002
Filed : January 14, 2003

REMARKS

Applicant wishes to thank Examiner Lucas and Interference Specialist Helms for the courtesy extended to Nancy Vensko, attorney of record, on April 10, 2006. The Interview Summary Form PTOL-413 summarizes the discussion held at the personal interview. The present response to the outstanding Office Action includes the substance of the Examiner Interview.

A. Disposition of Claims

Claims 1-8 and 11-18 are pending in this application. Claims 9, 10, and 19-40 have been canceled without prejudice as being drawn to non-elected subject matter. The claims have been amended so that application of the two-way test leads to the determination that USP 6,627,437 to Traboni and the claims of the present application do not define the same patentable invention. Additionally, Claims 6-8 and 11-14 have been edited to add "isolated" to define patentable subject matter as opposed to products of nature and to avoid accidental anticipation by Simons et al., Proc Natl Acad Sci USA 92: 3401, 1995. Support for the amendment is found throughout the specification, for example, at Table 1 and page 27, last sentence ("last 259 nucleotides"), and at page 16, lines 20-23 ("isolated"). No new matter has been added. Reexamination and reconsideration of the application, as amended, are respectfully requested.

B. Compliance with Rules regarding Nucleotide and/or Amino Acid Sequence Disclosures in Patent Applications

The specification has been amended to add sequence identifiers, and a new sequence listing in paper and computer readable form (CRF) submitted to conform thereto. Table 1 has been substituted with a replacement Table 1 to correct two typographical errors. The first is at position 2566 (should be T C C not ~~T-T-T~~). The second is at position 9061 (should be 9061 not 9067). Support for the amendment is found throughout the specification, for example, at original Table 1. This is because Table 1 illustrates the points of difference among GBV-B, GBV-B, 2/94, and pGBB. Table 1 explains that the sequence of GBV-B is that of Simons et al. 1995, of record, which gives the GenBank accession no. as U22304; the sequence of GBV-B, 2/94 is that of an intermediate clone; and the sequence of pGBB is that of the infectious clone, which is SEQ ID NO: 1. Exhibit 1 is a sequence alignment of SEQ ID NO: 1 and GenBank accession no.

Appl. No. : **10/009,002**
Filed : **January 14, 2003**

U22304. Exhibit 1 illustrates that position 2566 is C in the infectious clone, pGBB, not T, as in Simons et al. 1995. Additionally, Exhibit 1 illustrates that the position in the 3'UTR at which the infectious clone, pGBB, differs from Simons et al. 1995 by having a C, not T, is at position 9061, not 9067. Finally, Table 1 explains that the sequence of the intermediate clone, GBV-B, 2/94, is identical to that of the infectious clone, pGBB, except at the positions marked by an asterisk, thus we can deduce that positions 2566 and 9061 are identical for these two clones. In sum, the correction of the typographical errors in Table 1 does not introduce new matter as illustrated by sequence alignment of the infectious clone, pGBB, and Simons et al. 1995. (Please be notified that SEQ ID NO: 3 is identical to SEQ ID NO: 1 except for missing the last 259 nucleotides to illustrate the critical point of difference between the prior art and the infectious clone.) Finally, the correction of the typographical errors conforms Table 1 of the specification to the post-filing date inventor-created art of Bukh et al., Virology 262: 470, 1999, of record, at Table 1.

C. Compliance with 35 USC 101

The issue is whether Claims 6-8 and 11-14 are in compliance with 35 USC 101. These claims have been edited to add "isolated" to define patentable subject matter as opposed to products of nature. The conclusion is that the claims are in compliance with 35 USC 101.

D. Compliance with 35 USC 112/1

The issue is whether Claims 1, 4, 6-9, 11-13, and 15-17 are in compliance with 35 USC 112/1 as meeting the written description requirement. The claims have been amended so that application of the two-way test leads to the determination that USP 6,627,437 to Traboni and the claims of the present application do not define the same patentable invention. Comparing NIH (the present Applicant) and Traboni, the claims of the present application are directed to a species falling within the genus of Traboni in which NIH's 3'UTR is encoded by the last 259 nucleotides of SEQ ID NO: 1. Otherwise, for both Traboni and the present application, the remainder of the full-length clone is defined with reference to a GB virus-B that is infectious. Traboni is presumed to be valid. The 259 nucleotide 3'-end is identified in the present application as being required for infectivity and as solving the problem in the prior art of the lack of an infectious clone. The conclusion is that the claims of the present application, which are directed to a species falling within the genus of Traboni are in compliance with 35 USC 112/1.

Appl. No. : 10/009,002
Filed : January 14, 2003

E. Compliance with 35 USC 102(b)

The issue is whether Claims 8 and 11-13 are in compliance with 35 USC 102(b) or anticipated by Simons et al. 1995. The rule according to MPEP 2131 is that to anticipate a claim, the reference must teach every element of the claim. These claims have been edited to add “isolated” to avoid accidental anticipation by Simons et al. 1995. Simons et al. 1995 describes the non-infectious clone of the prior art missing the last 259 nucleotides. Simons et al. 1995 isolated the clone by converting nucleic acids extracted from preinoculation plasma or infectious plasma obtained from a GB-infected animal to double-stranded DNA by randomly primed RT and randomly primed second strand synthesis (Simon et al. 1995, p. 3402, col. 1, 1st ¶ of Results). The GB virus was not “isolated” just because it was found in plasma from a tamarin infected with the GB agent. The blood may have been *separated* to produce plasma. But the GB virus by itself was not *isolated*. Turning to the RNA, it was characterized and turned out to be missing the last 259 nucleotides. Ending with the host cell, it was not “isolated” either just because it was found in plasma from a tamarin infected with the GB agent. To reiterate, the blood may have been *separated* to produce plasma. But the host cell per se was not *isolated*. Please be informed that isolated RNA and host cells were patented in Traboni. Traboni is presumed to be valid. The conclusion is that Simons et al. 1995 fails to anticipate the claims, thus the claims are in compliance with 35 USC 102(b).

F. Separate Patentable Invention under 35 USC 102(g)

The issue is whether the claims define a separate patentable invention under 35 USC 102(g) or conflict with USP 6,627,437 to Traboni. The rule according to Eli Lilly & Co. v. Bd. of Regents of the Univ. of Wash., 67 USPQ2d 1161 (Fed. Cir. 2003) is that the two-way test is required for determining whether two parties claim the “same patentable invention”. A “separate patentable invention” means that the species invention of one party is new and nonobvious in view of the genus invention of the other party. Id. at p. 1164. The claims have been amended so that application of the two-way test leads to the determination that USP 6,627,437 to Traboni and the claims of the present application do not define the same patentable invention. The claims of the present application are directed to an isolated nucleic acid molecule which encodes GB virus-B having a complete 3’UTR and which is capable of producing infectious virus when transfected

Appl. No. : 10/009,002
Filed : January 14, 2003

into cells in vivo, wherein the 3'UTR is encoded by the last 259 nucleotides of SEQ ID NO: 1. USP 6,627,437 to Traboni describes a genus in which the 3'UTR is encoded by SEQ ID NO: 1 (the last 309 nucleotides of the full length clone), or SEQ ID NO: 2 (the last 259 nucleotides of the full length clone), and variations thereof having no more than 10 alterations and provided that each of said alterations is a substitution, addition, or deletion. Comparing NIH (the present Applicant) and Traboni, the claims of the present application are directed to a species falling within the genus of Traboni in which NIH's 3'UTR is encoded by the last 259 nucleotides of SEQ ID NO: 1. Otherwise, for both Traboni and the present application, the remainder of the full-length clone is defined with reference to a GB virus-B that is infectious. Exhibit 2 is a sequence alignment of the last 259 nucleotides of NIH's SEQ ID NO: 1 and the last 259 nucleotides of Traboni's SEQ ID NO: 1. Exhibit 2 illustrates that there is one point of difference between NIH's and Traboni's sequences.¹ NIH's species is not rendered obvious by Traboni's genus considering the size of the genus. Given that Traboni's 3'UTR sequence is encoded by 259 nucleotides and variations thereof having no more than 10 alterations and provided that each of said alterations is a substitution, addition, or deletion, the number of possibilities embraced by the Traboni genus is almost infinite. The number of possibilities is estimated by the following formula

$$\sum_{n=1}^{10} \frac{3^n 259!}{n! (259-n)!}$$

that equals on the order of 2×10^{22} . Absent anything in the prior art suggesting which of the almost infinite possibilities embraced by Traboni corresponds to NIH's 3'UTR, the prior art would not have suggested the claimed species. Although a genus may be so small that, when considered in light of the totality of the circumstances, it would anticipate the claimed species, not so here. Remembering that it embraces a number of possibilities that is almost infinite, the Traboni genus cannot inherently anticipate the claimed NIH species because one skilled in the art

¹ Please be reminded that U.S. 2004/0039187 to Martin et al. is not prior art in that it claims priority back to the same priority date as the present application and, as illustrated in Exhibit 2, there is one point of difference between NIH's and Martin et al.'s sequences.

Appl. No. : 10/009,002
Filed : January 14, 2003

would not envisage each member of the genus. Besides the size of the genus, a consideration of any teachings of a "typical" or "preferred" or "optimum" species within the disclosed genus reveals that any such teaching is nonexistent. Besides the size of the genus and lack of teachings to support the selection of the species, unexpected advantages reside in NIH's clone being fully infectious. Refer to specification at Example 3; accord, post-filing date inventor-created art of Bukh et al., Virology 262: 470, 1999, of record. Given the size of the genus, the lack of teachings to support the selection of the species, and the unexpected advantages, the conclusion is that the claims of the present application, which are directed to a species that is new and nonobvious in view of USP 6,627,437 to Traboni, define a separate patentable invention under 35 USC 102(g). No interference-in-fact exists.

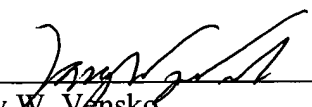
CONCLUSION

In view of the above, it is submitted that the claims are in condition for allowance. Reconsideration and withdrawal of all outstanding rejections are respectfully requested. Allowance of the claims at an early date is solicited. If any points remain that can be resolved by telephone, the Examiner is invited to contact the undersigned at the below-given telephone number.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: 5/1/06

By: 
Nancy W. Vensko
Registration No. 36,298
Attorney of Record
Customer No. 45,311
(805) 547-5580

AMEND

2538523
042006

EXHIBIT 1



Structure

Sbjct	121	GTAGGCGGCGGGACTCATGACGCTCGCGTGATGACAAGCGCCAAGCTTGA	180
Query	181	CCTGATGGGCGTTTCATGGGTTTCGGTGGTGGTGGCGCTTTAGGCAGCCTCCACGCCCACCA	240
Sbjct	181	CCTGATGGGCGTTTCATGGGTTTCGGTGGTGGTGGCGCTTTAGGCAGCCTCCACGCCCACCA	240
Query	241	CCTCCCAGATAGAGCGGCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACG	300
Sbjct	241	CCTCCCAGATAGAGCGGCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACG	300
Query	301	CAGACCTCTTTTTGAGTATCACGCCTCCGGAAGTAGTTGGGCAAGCCCACCTATATGTGT	360
Sbjct	301	CAGACCTCTTTTTGAGTATCACGCCTCCGGAAGTAGTTGGGCAAGCCCACCTATATGTGT	360
Query	361	TGGGATGGTTGGGGTTAGCCATCCATACCGTACTGCCTGATAGGGTCCTTGCGAGGGGAT	420
Sbjct	361	TGGGATGGTTGGGGTTAGCCATCCATACCGTACTGCCTGATAGGGTCCTTGCGAGGGGAT	420
Query	421	CTGGGAGTCTCGTAGACCGTAGCACATGCCTGTTATTTCTACTCAAACAAGTCCTGTACC	480
Sbjct	421	CTGGGAGTCTCGTAGACCGTAGCACATGCCTGTTATTTCTACTCAAACAAGTCCTGTACC	480
Query	481	TGCGCCCAAGACGCGCAAGAACAAGCAGACGCAGGCTTCATATCCTGTGTCCATTAAAAC	540
Sbjct	481	TGCGCCCAAGACGCGCAAGAACAAGCAGACGCAGGCTTCATATCCTGTGTCCATTAAAAC	540
Query	541	ATCTGTTGAAAGGGGACAACGAGCAAAGCGCAAAGTCCAGCGCGATGCTCGGCCTCGTAA	600
Sbjct	541	ATCTGTTGAAAGGGGACAACGAGCAAAGCGCAAAGTCCAGCGCGATGCTCGGCCTCGTAA	600
Query	601	TTACAAAATTGCTGGTATCCATGATGGCTTGCAGACATTGGCTCAGGCTGCTTTGCCAGC	660
Sbjct	601	TTACAAAATTGCTGGTATCCATGATGGCTTGCAGACATTGGCTCAGGCTGCTTTGCCAGC	660
Query	661	TCATGGTTGGGGACGCCAAGACCCTCGCCATAAGTCTCGCAATCTTGGAATCCTTCTGGA	720
Sbjct	661	TCATGGTTGGGGACGCCAAGACCCTCGCCATAAGTCTCGCAATCTTGGAATCCTTCTGGA	720
Query	721	TTACCCTTTGGGGTGGATTGGTGATGTTACAACCTCACACACCTCTAGTAGGCCCGCTGGT	780
Sbjct	721	TTACCCTTTGGGGTGGATTGGTGATGTTACAACCTCACACACCTCTAGTAGGCCCGCTGGT	780
Query	781	GGCAGGAGCGGTCGTTTCGACCAGTCTGCCAGATAGTACGCTTGCTGGAGGATGGAGTCAA	840
Sbjct	781	GGCAGGAGCGGTCGTTTCGACCAGTCTGCCAGATAGTACGCTTGCTGGAGGATGGAGTCAA	840
Query	841	CTGGGCTACTGGTTGGTTCGGTGTCCACCTTTTTGTGGTATGTCTGCTATCTTTGGCCTG	900
Sbjct	841	CTGGGCTACTGGTTGGTTCGGTGTCCACCTTTTTGTGGTATGTCTGCTATCTTTGGCCTG	900
Query	901	TCCCTGTAGTGGGGCGCGGGTCACTGACCCAGACACAAATACCACAATCCTGACCAATTG	960
Sbjct	901	TCCCTGTAGTGGGGCGCGGGTCACTGACCCAGACACAAATACCACAATCCTGACCAATTG	960
Query	961	CTGCCAGCGTAATCAGGTTATCTATTGTTCTCCTTCCACTTGCCCTACACGAGCCTGGTTG	1020
Sbjct	961	CTGCCAGCGTAATCAGGTTATCTATTGTTCTCCTTCCACTTGCCCTACACGAGCCTGGTTG	1020
Query	1021	TGTGATCTGTGCGGACGAGTGCTGGGTTCGCGCCAATCCGTACATCTCACACCCTTCCAA	1080

Sbjct	1021	TGTGATCTGCGCGGACGAGTGCTGGGTTCCTCGCCAATCCGTACATCTCACACCCTTCCAA	1080
Query	1081	TTGGACTGGCACGGACTCCTTCTTGGCTGACCACATTGATTTTGTTATGGGCGCTCTTGT	1140
Sbjct	1081	TTGGACTGGCACGGACTCCTTCTTGGCTGACCACATTGATTTTGTTATGGGCGCTCTTGT	1140
Query	1141	GACCTGTGACGCCCTTGACATTGGTGAGTTGTGTGGTGCGTGTGTATTAGTCGGTGACTG	1200
Sbjct	1141	GACCTGTGACGCCCTTGACATTGGTGAGTTGTGTGGTGCGTGTGTATTAGTCGGTGACTG	1200
Query	1201	GCTTGTGAGGCACTGGCTTATTACATAGACCTCAATGAACTGGTACTTGTTACCTGGA	1260
Sbjct	1201	GCTTGTGAGGCACTGGCTTATTACATAGACCTCAATGAACTGGTACTTGTTACCTGGA	1260
Query	1261	AGTGCCCACTGGAATAGATCCTGGGTTTCTAGGGTTTATCGGGTGGATGGCCGGCAAGGT	1320
Sbjct	1261	AGTGCCCACTGGAATAGATCCTGGGTTTCTAGGGTTTATCGGGTGGATGGCCGGCAAGGT	1320
Query	1321	CGAGGCTGTCATCTTCTTGACCAAAGTGGCTTCACAAGTACCATACGCTATTGCGACTAT	1380
Sbjct	1321	CGAGGCTGTCATCTTCTTGACCAAAGTGGCTTCACAAGTACCATACGCTATTGCGACTAT	1380
Query	1381	GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCCTCTCGGGGCAA	1440
Sbjct	1381	GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCCTCTCGGGGCAA	1440
Query	1441	GTGGTATCAGTTGCTCCTAGCGCTTATGCTTTACATAGAAGCGACCTCTGGAAACCCCAT	1500
Sbjct	1441	GTGGTATCAGTTGCTCCTAGCGCTTATGCTTTACATAGAAGCGACCTCTGGAAACCCCAT	1500
Query	1501	CAGGGTGCCCACTGGATGCTCAATAGCTGAGTTTTGCTCGCCTTTGATGATACCATGTCC	1560
Sbjct	1501	CAGGGTGCCCACTGGATGCTCAATAGCTGAGTTTTGCTCGCCTTTGATGATACCATGTCC	1560
Query	1561	TTGCCACTCTTATTTGAGTGAGAATGTGTCAGAAGTCATTTGTTACAGTCCAAAGTGGAC	1620
Sbjct	1561	TTGCCACTCTTATTTGAGTGAGAATGTGTCAGAAGTCATTTGTTACAGTCCAAAGTGGAC	1620
Query	1621	CAGGCCTATCACTCTAGAGTATAACAACCTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
Sbjct	1621	CAGGCCTATCACTCTAGAGTATAACAACCTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
Query	1681	TGCGAGGGGATGTATGGTTAAATTCAAAAATAACACATGGGGTTGCTGCCGTATTGCGAA	1740
Sbjct	1681	TGCGAGGGGATGTATGGTTAAATTCAAAAATAACACATGGGGTTGCTGCCGTATTGCGAA	1740
Query	1741	TGTGCCATCGTACTGCACTATGGGCACTGATGCAGTGTGGAACGACACTCGCAACACTTA	1800
Sbjct	1741	TGTGCCATCGTACTGCACTATGGGCACTGATGCAGTGTGGAACGACACTCGCAACACTTA	1800
Query	1801	CGAAGCATGCGGTGTAACACCATGGCTAACAACCGCATGGCACAACGGCTCAGCCCTGAA	1860
Sbjct	1801	CGAAGCATGCGGTGTAACACCATGGCTAACAACCGCATGGCACAACGGCTCAGCCCTGAA	1860
Query	1861	ATTGGCTATATTACAATACCCTGGGTCTAAAGAAATGTTTAAACCTCATAATTGGATGTC	1920
Sbjct	1861	ATTGGCTATATTACAATACCCTGGGTCTAAAGAAATGTTTAAACCTCATAATTGGATGTC	1920
Query	1921	AGGCCATTTGTATTTTGGGGATCAGATACCCCTATAGTTTACTTTTATGACCCTGTGAA	1980

Sbjct	1921	AGGCCATTTGTATTTTGGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCTGTGAA	1980
Query	1981	TTCCACTCTCCTACCACCGGAGAGGTGGGCTAGGTTGCCCAGTACCCACCTGTGGTACG	2040
Sbjct	1981	TTCCACTCTCCTACCACCGGAGAGGTGGGCTAGGTTGCCCAGTACCCACCTGTGGTACG	2040
Query	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGGTTTTACAGTGATGTGAAAGACCTAGCCACAGG	2100
Sbjct	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGGTTTTACAGTGATGTGAAAGACCTAGCCACAGG	2100
Query	2101	ATTGATCACCAAAGACAAAGCCTGGAAAAATTATCAGGTCTTATATTCCGCCACGGGTGC	2160
Sbjct	2101	ATTGATCACCAAAGACAAAGCCTGGAAAAATTATCAGGTCTTATATTCCGCCACGGGTGC	2160
Query	2161	TTTGTCTCTTACGGGAGTTACCACCAAGGCCGTGGTGCTAATTCTGTTGGGGTTGTGTGG	2220
Sbjct	2161	TTTGTCTCTTACGGGAGTTACCACCAAGGCCGTGGTGCTAATTCTGTTGGGGTTGTGTGG	2220
Query	2221	CAGCAAGTATCTTATTTTAGCCTACCTCTGTTACTTGTCCCTTTGTTTTGGGCGCGCTTC	2280
Sbjct	2221	CAGCAAGTATCTTATTTTAGCCTACCTCTGTTACTTGTCCCTTTGTTTTGGGCGCGCTTC	2280
Query	2281	TGGTTACCCTTTGCGTCCGTGTGCTCCCATCCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340
Sbjct	2281	TGGTTACCCTTTGCGTCCGTGTGCTCCCATCCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340
Query	2341	TTTGTCTAAAGCTCAAGTAGCTCCTTTTGCTTTGATTTTCTTCATCTGTTGCTATCTCCG	2400
Sbjct	2341	TTTGTCTAAAGCTCAAGTAGCTCCTTTTGCTTTGATTTTCTTCATCTGTTGCT	2400
Query	2401	CTGCAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGCGGG	2460
Sbjct	2401	CTGCAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGCGGGCTTGC	2460
Query	2461	AACTTTCTTTGTTGCAGCAGCTGCTGCCCAACCAGATTATGACTGGTGGGTCGACTGCT	2520
Sbjct	2461	AACTTTCTTTGTTGCAGCAGCTGCTGCCCAACCAGATTATGACTGGTGGTGGCGACTGCT	2520
Query	2521	AGTGGCAGGGTTAGTTTTGTGGGCCGGCCGTAACCGTGGTCACCGCATAGCTCTGCTTGT	2580
Sbjct	2521	AGTGGCAGGGTTAGTTTTGTGGGCCGGCCGTGACCGTGGTCCACGTATAGCTCTGCTTGT	2580
Query	2581	AGGTCCTTGGCCTCTGGTAGCGCTTTTAACCCTCTTGCATTTGGTTACGCCTGCTTCAGC	2640
Sbjct	2581	AGGTCCTTGGCCTCTGGTAGCGCTTTTAACCCTCTTGCATTTGGCTACGCCTGCTTCAGC	2640
Query	2641	TTTTGATACCGAGATAATTGGAGGGCTGACAATACCACCTGTAGTAGCATTAGTTGTCAT	2700
Sbjct	2641	TTTTGACACCGAGATAATTGGAGGGCTGACAATACCACCTGTAGTAGCATTAGTTGTCAT	2700
Query	2701	GTCTCGTTTTGGCTTCTTTGCTCACTTGTTACCTCGCTGTGCTTTAGTTAACTCCTATCT	2760
Sbjct	2701	GTCTCGTTTTGGCTTCTTTGCTCACTTGTTACCTCGCTGTGCTTTAGTTAACTCCTATCT	2760
Query	2761	TTGGCAACGTTGGGAGAATTGGTTTTTGAACGTTACACTAAGACCGGAGAGGTTTTTCCT	2820
Sbjct	2761	TTGGCAACGTTGGGAGAATTGGTTTTTGAACGTTACACTAAGACCGGAGAGGTTTTTCCT	2820
Query	2821	TGTGCTGGTTTTGTTTTCCCGGTGCGACATATGACGCGCTGGTGACTTTCTGTGTGTGTCA	2880

NOTE

Sbjct	2821	TGTGCTGGTTTGTTCCTCCCGGTGCGACATATGACACGCTGGTGACTTTCTGTGTGTGTCA	2880
Query	2881	CGTAGCTCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGT	2940
Sbjct	2881	CGTAGCTCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGT	2940
Query	2941	TAGGGCCCATAGAATGTTGGTGCGTCTCGGAAAGTGTCATGCTTGGTATTCTCATTATGT	3000
Sbjct	2941	TAGGGCCCATAGAATGTTGGTGCGTCTCGGAAAGTGTCATGCTTGGTATTCTCATTATGT	3000
Query	3001	TCTTAAGTTTTTCTCTTAGTGTTTGGTGAGAATGGTGTGTTTTTCTATAAGCACTTGCA	3060
Sbjct	3001	TCTTAAGTTTTTCTCTTAGTGTTTGGTGAGAATGGTGTGTTTTTCTATAAGCACTTGCA	3060
Query	3061	TGGTGATGTCTTGCCTAATGATTTTGCCTCGAAACTACCATTGCAAGAGCCATTTTTCCC	3120
Sbjct	3061	TGGTGATGTCTTGCCTAATGATTTTGCCTCGAAACTACCATTGCAAGAGCCATTTTTCCC	3120
Query	3121	TTTTGAAGGCAAGGCAAGGGTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
Sbjct	3121	TTTTGAAGGCAAGGCAAGGGTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
Query	3181	GGTTGATGGTTTGCCCGTTGTTGCGCGTCTCGGCGACCTTGTTTTCGCAGGGTTGGCTAT	3240
Sbjct	3181	GGTTGATGGTTTGCCCGTTGTTGCGCGTCTCGGCGACCTTGTTTTCGCAGGGTTAGCTAT	3240
Query	3241	GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300
Sbjct	3241	GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300
Query	3301	CACGCTGTCAGCGATGGCAGTGGTCATGACTGGTATAGACCCCGAACTTGGACTGGAAC	3360
Sbjct	3301	CACGCTGTCAGCGATGGCAGTGGTCATGACTGGTATAGACCCCGAACTTGGACTGGAAC	3360
Query	3361	TATCTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGATTGTTTGTGACAACGTGTT	3420
Sbjct	3361	TATCTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGATTGTTTGTGACAACGTGTT	3420
Query	3421	GTATACTGCTCACCATGGCAGCAAGGGGCGCCGGTTGGCTCATCCACAGGCTCTATACA	3480
Sbjct	3421	GTATACTGCTCACCATGGCAGCAAGGGGCGCCGGTTGGCTCATCCACAGGCTCCATACA	3480
Query	3481	CCCAATAACCGTTGACGCGGCTAATGACCAGGACATCTATCAACCACCATGTGGAGCTGG	3540
Sbjct	3481	CCCAATAACCGTTGACGCGGCTAATGACCAGGACATCTATCAACCACCATGTGGAGCTGG	3540
Query	3541	GTCCCTTACTCGGTGCTCTTGCGGGGAGACCAAGGGGTATCTGGTAACACGACTGGGGTC	3600
Sbjct	3541	GTCCCTTACTCGGTGCTCTTGCGGGGAGACCAAGGGGTATCTGGTAACACGACTGGGGTC	3600
Query	3601	ATTGGTTGAGGTCAACAAATCCGATGACCTTATTGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Sbjct	3601	ATTGGTTGAGGTCAACAAATCCGATGACCTTATTGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Query	3661	GGCTGTTGCCAAGGGTTCTTCAGGTGCCCCGATTCTGTGCTCCTCCGGGCATGTTATTGG	3720
Sbjct	3661	GGCTGTTGCCAAGGGTTCTTCAGGTGCCCCGATTCTGTGCTCCTCCGGGCATGTTATTGG	3720
Query	3721	GATGTTACCGCTGCTAGAAATTCTGGCGGTTCAGTCAGTCAGATTAGGGTTAGGCCGTT	3780

Sbjct	3721	GATGTTACCGCTGCTAGAAATTCTGGCGGTTTCAGTCAGCCAGATTAGGGTTAGGCCGTT	3780
Query	3781	GGTGTGTGCTGGATACCATCCCCAGTACACAGCACATGCCACTCTTGATACAAAACCTAC	3840
Sbjct	3781	GGTGTGTGCTGGATACCATCCCCAGTACACAGCACATGCCACTCTTGATACAAAACCTAC	3840
Query	3841	TGTGCCTAACGAGTATTTCAGTGCAAATTTTAATTGCCCCACTGGCAGCGGCAAGTCAAC	3900
Sbjct	3841	TGTGCCTAACGAGTATTTCAGTGCAAATTTTAATTGCCCCACTGGCAGCGGCAAGTCAAC	3900
Query	3901	CAAATTACCACTTTCTTACATGCAGGAGAAGTATGAGGTCTTGGTCCTAAATCCCAGTGT	3960
Sbjct	3901	CAAATTACCACTTTCTTACATGCAGGAGAAGTATGAGGTCTTGGTCCTAAATCCCAGTGT	3960
Query	3961	GGCTACAACAGCATCAATGCCAAAGTACATGCACGCGACGTACGGCGTGAATCCAAATTG	4020
Sbjct	3961	GGCTACAACAGCATCAATGCCAAAGTACATGCACGCGACGTACGGCGTGAATCCAAATTG	4020
Query	4021	CTATTTTAATGGCAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT	4080
Sbjct	4021	CTATTTTAATGGCAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT	4080
Query	4081	GTACCTGACCGGAGCATGTTCCCGGAACATGATGTAATCATTGTGACGAATGCCATGC	4140
Sbjct	4081	GTACCTGACCGGAGCATGTTCCCGGAACATGACGTCATCATTGTGACGAATGCCATGC	4140
Query	4141	TACCGATGCAACCACCGTGTTGGGCATTGGAAAGGTCTAACCGAAGCTCCATCCAAAAA	4200
Sbjct	4141	TACCGATGCAACCACCGTGTTGGGCATTGGAAAGGTCTAACCGAAGCTCCATCCAAAAA	4200
Query	4201	TGTTAGGCTAGTGGTTCTTGCCACGGCTACCCCCCTGGAGTAATCCCTACACCACATGC	4260
Sbjct	4201	TGTTAGGCTAGTGGTTCTTGCCACGGCTACCCCCCTGGAGTAATCCCTACACCACATGC	4260
Query	4261	CAACATAACTGAGATTCAATTAACCGATGAAGGCACTATCCCCTTTCATGGAAAAAAGAT	4320
Sbjct	4261	CAACATAACTGAGATTCAATTAACCGATGAAGGCACTATCCCCTTTCATGGAAAAAAGAT	4320
Query	4321	TAAGGAGGAAAATCTGAAGAAAGGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
Sbjct	4321	TAAGGAGGAAAATCTGAAGAAAGGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
Query	4381	TGATGAGCTTGCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
Sbjct	4381	TGATGAGCTTGCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
Query	4441	ATGTGACATCTCAAAAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCCTTGTG	4500
Sbjct	4441	ATGTGACATCTCAAAAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCCTTGTG	4500
Query	4501	TACAGGGTACACTGGTGACTTTGATTCCGTGTATGACTGCAGCCTCATGGTAGAAGGCAC	4560
Sbjct	4501	TACAGGGTACACTGGTGACTTTGATTCCGTGTATGACTGCAGCCTCATGGTAGAAGGCAC	4560
Query	4561	ATGCCATGTTGACCTTGACCCTACTTTACCATGGGTGTTTCGTGTGTGCGGGGTTTCAGC	4620
Sbjct	4561	ATGCCATGTTGACCTTGACCCTACTTTACCATGGGTGTTTCGTGTGTGCGGGGTTTCAGC	4620
Query	4621	AATAGTTAAAGGCCAGCGTAGGGGCCGCACAGGCCGTGGGAGAGCTGGCATATACTACTA	4680

Sbjct	4621	AATAGTTAAAGGCCAGCGTAGGGGCCGCACAGGCCGTGGGAGAGCTGGCATATACTACTA	4680
Query	4681	TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCCTGAATGCAACATTGTTGAAGCCTT	4740
Sbjct	4681	TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCCTGAATGCAACATTGTTGAAGCCTT	4740
Query	4741	CGACGCAGCCAAGGCATGGTATGGTTTGTTCATCAACAGAAGCTCAAACATTCTGGACAC	4800
Sbjct	4741	CGACGCAGCCAAGGCATGGTATGGTTTGTTCATCAACAGAAGCTCAAACATTCTGGACAC	4800
Query	4801	CTATCGCACCCAACCTGGGTTACCTGCGATAGGAGCAAATTTGGACGAGTGGGCTGATCT	4860
Sbjct	4801	CTATCGCACCCAACCTGGGTTACCTGCGATAGGAGCAAATTTGGACGAGTGGGCTGATCT	4860
Query	4861	CTTTTCTATGGTCAACCCCGAACCTTCATTTGTCAATACTGCAAAAAGAACTGCTGACAA	4920
Sbjct	4861	CTTTTCTATGGTCAACCCCGAACCTTCATTTGTCAATACTGCAAAAAGAACTGCTGACAA	4920
Query	4921	TTATGTTTTGTTGACTGCAGCCCAACTACAACGTGTGCATCAGTATGGCTATGCTGCTCC	4980
Sbjct	4921	TTATGTTTTGTTGACTGCAGCCCAACTACAACGTGTGCATCAGTATGGCTATGCTGCTCC	4980
Query	4981	CAATGACGCACCACGGTGGCAGGGAGCCCGCTTGGGAAAAAACCTTGTGGGGTTCTGTG	5040
Sbjct	4981	CAATGACGCACCACGGTGGCAGGGAGCCCGCTTGGGAAAAAACCTTGTGGGGTTCTGTG	5040
Query	5041	GCGCTTGGACGGCGCTGACGCCTGTCCTGGCCCAGAGCCCAGCGAGGTGACCAGATACCA	5100
Sbjct	5041	GCGCTTGGACGGCGCTGACGCCTGTCCTGGCCCAGAGCCCAGCGAGGTGACCAGATACCA	5100
Query	5101	AATGTGCTTCACTGAAGTCAATACTTCTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT	5160
Sbjct	5101	AATGTGCTTCACTGAAGTCAATACTTCTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT	5160
Query	5161	GGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGCGGCGTTGCTGGTC	5220
Sbjct	5161	GGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGCGGCGTTGCTGGTC	5220
Query	5221	TATTACATCAGTCCCTACCGGTGCTACTGTCGCCCCAGTGGTTGACGAAGAAGAAATCGT	5280
Sbjct	5221	TATTACATCAGTCCCTACCGGTGCTACTGTCGCCCCAGTGGTTGACGAAGAAGAAATCGT	5280
Query	5281	GGAGGAGTGTGCATCATTCATTCCCTTGGAGGCCATGGTTGCTGCAATTGACAAGCTGAA	5340
Sbjct	5281	GGAGGAGTGTGCATCATTCATTCCCTTGGAGGCCATGGTTGCTGCAATCGATAAGCTGAA	5340
Query	5341	GAGTACAATCACCACTAGTCCTTTTACATTGGAAACCGCCCTTGAAAACTTAACAC	5400
Sbjct	5341	GAGTACAATAACCACACTAGTCCTTTTACATTGGAAACCGCCCTTGAAAACTTAACAC	5400
Query	5401	CTTTCTTGGGCCTCATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGTTAGT	5460
Sbjct	5401	CTTTCTTGGGCCTCATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGCTTAGT	5460
Query	5461	CACTTTACCTGACAATCCCTTTGCATCATGCGTGTGCTTTTATTGCGGGTATTACTAC	5520
Sbjct	5461	CACTTTACCTGACAATCCCTTTGCATCATGCGTGTGCTTTTATTGCGGGTATTACTAC	5520
Query	5521	CCCACTACCTCACAAGATCAAAATGTTTCTGTATTATTTGGAGGCGCAATTGCGTCCAA	5580

Sbjct	5521	CCCACTACCTCACAAGATCAAATGTTCTGTCTATTATTTGGAGGCGCAATTGCGTCCAA	5580
Query	5581	GCTTACAGACGCTAGAGGCGCACTGGCGTTCATGATGGCCGGGGCTGCGGGAACAGCTCT	5640
Sbjct	5581	GCTTACAGACGCTAGAGGCGCACTGGCGTTCATGATGGCCGGGGCTGCGGGAACAGCTCT	5640
Query	5641	TGGTACATGGACATCGGTGGGTTTTGTCTTTGACATGCTAGGCGGCTATGCTGCCGCCTC	5700
Sbjct	5641	TGGTACATGGACATCGGTGGGTTTTGTCTTTGACATGCTAGGCGGCTATGCTGCCGCCTC	5700
Query	5701	ATCCACTGCTTGCTTGACATTTAAATGCTTGATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Sbjct	5701	ATCCACTGCTTGCTTGACATTTAAATGCTTGATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Query	5761	TGCTGGTTTAGTCTACTCCGCGTTCAATCCGGCCGCGAGGAGTTGTGGGCGTCTTGTCAGC	5820
Sbjct	5761	TGCTGGTTTAGTCTACTCCGCGTTCAATCCGGCCGCGAGGAGTTGTGGGCGTCTTGTCAGC	5820
Query	5821	TTGTGCAATGTTTGCTTTGACAACAGCAGGGCCAGATCACTGGCCCAACAGACTTCTTAC	5880
Sbjct	5821	TTGTGCAATGTTTGCTTTGACAACAGCAGGGCCAGATCACTGGCCCAACAGACTTCTTAC	5880
Query	5881	TATGCTTGCTAGGAGCAACACTGTATGTAATGAGTACTTTATTGCCACTCGTGACATCCG	5940
Sbjct	5881	TATGCTTGCTAGGAGCAACACTGTATGTAATGAGTACTTTATTGCCACTCGTGACATCCG	5940
Query	5941	CAGGAAGATACTGGGCATTCTGGAGGCATCTACCCCCTGGAGTGTCATATCAGCTTGCA	6000
Sbjct	5941	CAGGAAGATACTGGGCATTCTGGAGGCATCTACCCCCTGGAGTGTCATATCAGCTTGCA	6000
Query	6001	CCGTTGGCTCCACACCCCGACGGAGGATGATTGCGGCCTCATTGCTTGGGGTCTAGAGAT	6060
Sbjct	6001	CCGTTGGCTCCACACCCCGACGGAGGATGATTGCGGCCTCATTGCTTGGGGTCTAGAGAT	6060
Query	6061	TTGGCAGTATGTGTGCAATTTCTTTGTGATTTGCTTTAATGTCCTTAAAGCTGGAGTTCA	6120
Sbjct	6061	TTGGCAGTATGTGTGCAATTTCTTTGTGATTTGCTTTAATGTCCTTAAAGCTGGAGTTCA	6120
Query	6121	GAGCATGGTTAACATTCTGGTTGTCCTTTCTACAGCTGCCAGAAGGGGTACAAGGGCCC	6180
Sbjct	6121	GAGCATGGTTAACATTCTGGTTGTCCTTTCTACAGCTGCCAGAAGGGGTACAAGGGCCC	6180
Query	6181	CTGGATTGGATCAGGTATGCTCCAAGCACGCTGTCCATGCGGTGCTGAACTCATCTTTTC	6240
Sbjct	6181	CTGGATTGGATCAGGTATGCTCCAAGCACGCTGTCCATGCGGTGCTGAACTCATCTTTTC	6240
Query	6241	TGTTGAGAATGGTTTTGCAAACTTTACAAAGGACCCAGAACTTGTTCAAATTACTGGAG	6300
Sbjct	6241	TGTTGAGAATGGTTTTGCAAACTTTACAAAGGACCCAGAACTTGTTCAAATTACTGGAG	6300
Query	6301	AGGGGCTGTTCCAGTCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCAACTGATTG	6360
Sbjct	6301	AGGGGCTGTTCCAGTCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCAACTGATTG	6360
Query	6361	GACTAGTCTTGTCGTCAATTATGGCGTTAGGGACTACTGTAAATATGAGAAAATGGGAGA	6420
Sbjct	6361	GACTAGTCTTGTCGTCAATTATGGCGTTAGGGACTACTGTAAATATGAGAAAATGGGAGA	6420
Query	6421	TCACATTTTTGTTACAGCAGTATCCTCTCAAATGTCTGTTTCACCCAGGTGCCCCAAC	6480

Sbjct	6421	TCACATTTTTGTTACAGCAGTATCCTCTCCAAATGTCTGTTTCACCCAGGTGCCCCAAC	6480
Query	6481	CTTGAGAGCTGCAGTGGCCGTGGACGGCGTACAGGTTCAAGTGTATCTAGGTGAGCCCCAA	6540
Sbjct	6481	CTTGAGAGCTGCAGTGGCCGTGGACGGCGTACAGGTTCAAGTGTATCTAGGTGAGCCCCAA	6540
Query	6541	AACTCCTTGGACGACATCTGCTTGCTGTTACGGTCCTGACGGTAAGGGTAAAAGTGTAA	6600
Sbjct	6541	AACTCCTTGGACGACATCTGCTTGCTGTTACGGTCCTGACGGTAAGGGTAAAAGTGTAA	6600
Query	6601	GCTTCCCTTCCGCGTTGACGGTCACACACCTGGTGTGCGCATGCAACTTAATTTGCGTGA	6660
Sbjct	6601	GCTTCCCTTCCGCGTTGACGGTCACACACCTGGTGTGCGCATGCAACTTAATTTGCGTGA	6660
Query	6661	TGCACTTGAGACAAATGACTGTAATTCACAAACAACACTCCTAGTGATGAAGCCGCAGT	6720
Sbjct	6661	TGCACTTGAGACAAATGACTGTAATTCATAAACAACACTCCTAGTGATGAAGCCGCAGT	6720
Query	6721	GTCCGCTCTTGTTTTCAAACAGGAGTTGCGGCGTACAAACCAATTGCTTGAGGCAATTTTC	6780
Sbjct	6721	GTCCGCTCTTGTTTTCAAACAGGAGTTGCGGCGTACAAACCAATTGCTTGAGGCAATTTTC	6780
Query	6781	AGCTGGCGTTGACACCACCAAAGTCCAGCCCCCTCCATCGAAGAGGTAGTGGTAAGAAA	6840
Sbjct	6781	AGCTGGCGTTGACACCACCAAAGTCCAGCCCCCTCCATCGAAGAGGTAGTGGTAAGAAA	6840
Query	6841	GCGCCAGTTCCGGGCAAGAACTGGTTCGCTTACCTTGCCCTCCCCCTCCGAGATCCGTCCC	6900
Sbjct	6841	GCGCCAGTTCCGGGCAAGAACTGGTTCGCTTACCTTGCCCTCCCCCTCCGAGATCCGTCCC	6900
Query	6901	AGGAGTGTCATGTCCTGAAAGCCTGCAACGAAGTGACCCGTTAGAAGGTCCTTCAAACCT	6960
Sbjct	6901	AGGAGTGTCATGTCCTGAAAGCCTGCAACGAAGTGACCCGTTAGAAGGTCCTTCAAACCT	6960
Query	6961	CCCTCCTTCACCACCTGTTCTACAGTTGGCCATGCCGATGCCCTGTTGGGAGCGGGTGA	7020
Sbjct	6961	CCCTCCTTCACCACCTGTTCTACAGTTGGCCATGCCGATGCCCTGTTGGGAGCAGGTGA	7020
Query	7021	GTGTAACCCTTTCACTGCAATTGGATGTGCAATGACCGAAACAGGCGGAGGCCCTGATGA	7080
Sbjct	7021	GTGTAACCCTTTCACTGCAATTGGATGTGCAATGACCGAAACAGGCGGAGGCCCTGATGA	7080
Query	7081	TTTACCCAGTTACCCTCCCAAAAAGGAGGTCTCTGAATGGTCAGACGAAAGTTGGTCAAC	7140
Sbjct	7081	TTTACCCAGTTACCCTCCCAAAAAGGAGGTCTCTGAATGGTCAGACGGAAGTTGGTCAAC	7140
Query	7141	GGCTACAACCGCTTCCAGCTACGTTACTGGCCCCCGTACCCTAAGATACGGGGAAAGGA	7200
Sbjct	7141	GACTACAACCGCTTCCAGCTACGTTACTGGCCCCCGTACCCTAAGATACGGGGAAAGGA	7200
Query	7201	TTCCACTCAGTCAGCCCCCGCCAAACGGCCTACAAAAAGAAGTTGGGAAAGAGTGAGTT	7260
Sbjct	7201	TTCCACTCAGTCAGCCCCCGCCAAACGGCCTACAAAAAGAAGTTGGGAAAGAGTGAGTT	7260
Query	7261	TTCGTGCAGCATGAGCTACACCTGGACCGACGTGATTAGCTTCAAACTGCTTCTAAAGT	7320
Sbjct	7261	TTCGTGCAGCATGAGCTACACTGGACCGACGTGATTAGCTTCAAACTGCTTCTAAAGT	7320
Query	7321	TCTGTCTGCAACTCGGGCCATCACTAGTGGTTTCCTCAAACAAAGATCATTGGTGTATGT	7380

Sbjct	7321	TCTGTCTGCAACTCGGGCCATCACTAGTGGTTTCCTCAAACAAAGATCATTGGTGTATGT	7380
Query	7381	GACTGAGCCGCGGGATGCGGAGCTTAGAAAACAAAAGTCACTATTAATAGACAACCTCT	7440
Sbjct	7381	GACTGAGCCGCGGGATGCGGAGCTTAGAAAACAAAAGTCACTATTAATAGACAACCTCT	7440
Query	7441	GTTCCCCCATCATACCACAAGCAAGTGAGATTGGCTAAGGAAAAAGCTTCAAAGTTGT	7500
Sbjct	7441	GTTCCCCCATCATACCACAAGCAAGTGAGATTGGCTAAGGAAAAAGCTTCAAAGTTGT	7500
Query	7501	CGGTGTCATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAGTC	7560
Sbjct	7501	CGGTGTCATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAGTC	7560
Query	7561	CCACATCACTGGCCTTCGGGGCACTGATGTTTCGTTCTGGAGCAGCCGCAAGGCTGTTCT	7620
Sbjct	7561	CCACATCACTGGCCTTCGGGGCACTGATGTTTCGTTCTGGAGCAGCCGCAAGGCTGTTCT	7620
Query	7621	GGACTTGCAGAAGTGTGTCGAGGCAGGTGAGATACCGAGTCATTATCGGCAAACCTGTGAT	7680
Sbjct	7621	GGACTTGCAGAAGTGTGTCGAGGCAGGTGAGATACCGAGTCATTATCGGCAAACCTGTGAT	7680
Query	7681	AGTTCCAAAGGAGGAGGTCTTCGTGAAGACCCCCAGAAACCAACAAAGAAACCCCAAG	7740
Sbjct	7681	AGTTCCAAAGGAGGAGGTCTTCGTGAAGACCCCCAGAAACCAACAAAGAAACCCCAAG	7740
Query	7741	GCTTATCTCGTACCCCCACCTTGAAATGAGATGTGTTGAGAAGATGTACTACGGTCAGGT	7800
Sbjct	7741	GCTTATCTCGTACCCCCACCTTGAAATGAGATGTGTTGAGAAGATGTACTACGGTCAGGT	7800
Query	7801	TGCTCCTGACGTAGTTAAAGCTGTCATGGGAGATGCGTACGGGTTTGTAGATCCACGTAC	7860
Sbjct	7801	TGCTCCTGACGTAGTTAAAGCTGTCATGGGAGATGCGTACGGGTTTGTGACCCACGTAC	7860
Query	7861	CCGTGTCAAGCGTCTGTTGTCGATGTGGTCACCCGATGCAGTCGGAGCCACATGCGATAC	7920
Sbjct	7861	CCGTGTCAAGCGTCTGTTGTCGATGTGGTCACCCGATGCAGTCGGAGCCACATGCGATAC	7920
Query	7921	AGTGTGTTTTTGACAGTACCATCACACCCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Sbjct	7921	AGTGTGTTTTTGACAGTACCATCACACCCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Query	7981	AGCAGCTAAACTCAGTGACCAACACCGAGCTGGCATTACACCATTGCGAGGCAGTTATA	8040
Sbjct	7981	AGCAGCTAAACTCAGTGACCAACACCGAGCTGGCATTACACCATTGCGAGGCAGTTATA	8040
Query	8041	CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTGTAGGTC	8100
Sbjct	8041	CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTGTAGGTC	8100
Query	8101	TTCCGGCGTCTATACTACCTCAAGTTCCAACAGTTTGACCTGCTGGCTGAAGGTAAATGC	8160
Sbjct	8101	TTCCGGCGTCTATACTACCTCAAGTTCCAACAGTTTGACCTGCTGGCTGAAGGTAAATGC	8160
Query	8161	TGCAGCCGAACAGGCTGGCATGAAGAACCCTCGCTTCCTTATTTGCGGCGATGATTGCAC	8220
Sbjct	8161	TGCAGCCGAACAGGCTGGCATGAAGAACCCTCGCTTCCTTATTTGCGGCGATGATTGCAC	8220
Query	8221	CGTAATTTGGAAGAGCGCCGGAGCAGATGCAGACAAACAAGCAATGCGTGTCTTTGCTAG	8280

Sbjct	8221	CGTAATTTGGAAGAGCGCCGGAGCAGATGCAGACAAACAAGCAATGCGTGTCTTTGCTAG	8280
Query	8281	CTGGATGAAGGTGATGGGTGCACCACAAGATTGTGTGCCTCAACCCAAATACAGTTTGA	8340
Sbjct	8281	CTGGATGAAGGTGATGGGTGCACCACAAGATTGTGTGCCTCAACCCAAATACAGTTTGA	8340
Query	8341	AGAATTAACATCATGCTCATCAAATGTTACCTCTGGAATTACCAAAAGTGGCAAGCCTTA	8400
Sbjct	8341	AGAATTAACATCATGCTCATCAAATGTTACCTCTGGAATTACCAAAAGTGGCAAGCCTTA	8400
Query	8401	CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Sbjct	8401	CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Query	8461	ATACAACCCCAGTGCTGCGTGGATTGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
Sbjct	8461	ATACAACCCCAGTGCTGCGTGGATTGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
Query	8521	TAGCCGTGTGTTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Sbjct	8521	TAGCCGTGTGTTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Query	8581	GACTGTGACCTTTGACTGGTATGGGAAAAATTATACGGTGCCTGTAGAAGATCTGCCCAG	8640
Sbjct	8581	GACTGTGACCTTTGACTGGTATGGGAAAAATTATACGGTGCCTGTAGAAGATCTGCCCAG	8640
Query	8641	CATCATTGCTGGTGTGCACGGTATTGAGGCTTTCTCGGTGGTGCCTACACCAACGCTGA	8700
Sbjct	8641	CATCATTGCTGGTGTGCACGGTATTGAGGCTTTCTCGGTGGTGCCTACACCAACGCTGA	8700
Query	8701	GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCCCCTGCGAGCCTGGCG	8760
Sbjct	8701	GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCCCCTGCGAGCCTGGCG	8760
Query	8761	AAAGAAAGCCAGGGCGGTCTCGCCAGCGCCAAGAGGCGTGGCGGAGCACACGCAAAATT	8820
Sbjct	8761	AAAGAAAGCCAGGGCGGTCTCGCCAGCGCCAAGAGGCGTGGCGGAGCACACGCAAAATT	8820
Query	8821	GGCTCGCTTCCTTCTCTGGCATGCTACATCTAGACCTCTACCAGATTTGGATAAGACGAG	8880
Sbjct	8821	GGCTCGCTTCCTTCTCTGGCATGCTACATCTAGACCTCTACCAGATTTGGATAAGACGAG	8880
Query	8881	CGTGGCTCGGTACACCACTTTCAATTATTGTGATGTTTACTCCCCGAGGGGGATGTGTT	8940
Sbjct	8881	CGTGGCTCGGTACCACTTTCAATTATTGTGATGTTTACTCCCCGAGGGGGATGTGTT	8940
Query	8941	TATTACA. TATTGCAGAAGTTCCTTGTGAAGTATTTGGCTGTCATTGTTTT	9000
Sbjct	8941	TGTTACACCAC. TATTGCAGAAGTTCCTTGTGAAGTATTTGGCTGTCATTGTTTT	9000
Query	9001	TGCCCCAGGGGCTCATTGCTGTTGGATTAGCCATCAGCTGAACCCCCAAATTCAAATTAA	9060
Sbjct	9001	TGCCCCAGGGGCTCATTGCTGTTGGATTAGCCATCAGCTGAACCCCCAAATTCAAATTAA	9060
Query	9061	CTAACAG----TTTTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGGCAACAGGGGAGACCCC	9116
Sbjct	9061	TTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGGCAACAGGGGAGACCCC	9120
Query	9117	GGGCTTAACGACCCCGC	9133

NOTE

Sbjct 9121 GGGCTTAACGACCCCGC 9137

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 1

Number of Hits to DB: 4626

Number of extensions: 85

Number of successful extensions: 19

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 9399

Length of database: 17,071,139,809

Length adjustment: 28

Effective length of query: 9371

Effective length of database: 17,071,139,781

Effective search space: 159973650887751

Effective search space used: 159973650887751

X1: 11 (21.1 bits)

X2: 26 (50.0 bits)

X3: 26 (50.0 bits)

S1: 16 (31.5 bits)

S2: 23 (44.9 bits)

EXHIBIT 2

Sequence Alignment

NIH vs. Traboni

NIH	1	AGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATG	60
Traboni	1	AGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATG	60
NIH	61	ACGTCCCTTCTGGCTCATCCACAAAAACCGTCTCGGGTGGGTGAGGAGTCCTGGCTGTGT	120
Traboni	61	ACGTCCCTTCTGGCTCATCCACAAAAACCGTCTCGGGTGGGTGAGGAGTCCTGGCTGTGT	120
NIH	121	GGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTATTTGTCCGC	180
Traboni	121	GGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTACTTGTCCGC	180
NIH	181	TGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCGAAGCGGAGGGCAACCC	240
Traboni	181	TGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCGAAGCGGAGGGCAACCC	240
NIH	241	CCGCTTGGAATTAAAAACT	259
Traboni	241	CCGCTTGGAATTAAAAACT	259

NIH vs. Martin

NIH	1	AGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATG	60
Martin	1	GAGTTTG-CGACCATGGTGGATCAGAACCGTTTCGGGTGAAGCCATGGTCTGAAGGGGATG	60
NIH	61	ACGTCCCTTCTGGCTCATCCACAAAAACCGTCTCGGGTGGGTGAGGAGTCCTGGCTGTGT	120
Martin	61	ACGTCCCTTCTGGCTCATCCACAAAAACCGTCTCGGGTGGGTGAGGAGTCCTGGCTGTGT	120
NIH	121	GGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTATTTGTCCGC	180
Martin	121	GGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGCCTCACGACGTATTTGTCCGC	180
NIH	181	TGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCGAAGCGGAGGGCAACCC	240
Martin	181	TGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTGTTCGAAGCGGAGGGCAACCC	240
NIH	241	CCGCTTGGAATTAAAAACT	259
Martin	241	CCGCTTGGAATTAAAAACTG	260